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 <140> PCT/US99/31169
 <141> 1999-12-30
 <150> 09/224,426
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tgggagcagg cgaccggcac tggctggatg gacctggaag cctcgctgct gcccactqqt 240
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Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met 100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly 165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser 225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe 245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr 260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu 275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met 290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr 305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val 325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser 340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu 355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys 370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln 385 390 395 400

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gggcatcgtg ggaaactcca cggtcatctt tgctgtggtg aagaagtcca agctacactg 240
gtgcagcaac gtccccgaca tcttcatcat caacctctct gtggtggatc tgctcttcct 300
getgggeatg cettteatga tecaceaget eatggggaae ggegtetgge aetttgggga 360
aaccatgtgc accctcatca cagccatgga cgccaacagt cagttcacta gcacctacat 420
cctgactgcc atgaccattg accgctactt ggccaccgtc cacccatct cctccaccaa 480
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tttcctggcc tttgcccttc cgtttgtggt cattaccgcc gcatacgtga aaatactaca 720
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caacgcggcc atcagcttgg gctatgctaa cagctgcctg aacccctttg tgtacatagt 960
getetgtgag acetttegaa aaegettggt gttgteagtg aageetgeag eecaggggea 1020
gctccgcacg gtcagcaacg ctcagacagc tgatgaggag aggacagaaa gcaaaggcac 1080
ctgacaattc cccagtcgcc tccaagtcag gccaccccat caaaccgtgg ggagagatac 1140
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. 35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala 50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile 65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met 85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly 100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe 115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala 130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala 145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr 165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val 180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe 195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile 210 215 220

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala 225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg 245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr 260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr 275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser 290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys 305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr 325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly 340 345 350

Thr

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<210> 9	
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cgcggaccca coacycray y y	
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(772) Description of Withington Bedgoude. Mitmot/Mind.	
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<211> 29
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Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro

<210> 17

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human MCH1

<400> 17

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu 1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

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Gly Ser Pro Pro
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Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
                                                  45
         35
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
                         55
     50
Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
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                     70
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Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
                                105
            100
Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
                            120
                                                125
        115
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
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24

135

130

140

Asn 145	Val	Pro	Asp	Ile	Phe 150	Ile	Ile	Asn	Leu	Ser 155	Val	Val	Asp	Leu	Leu 160
Phe	Leu	Leu	Gly	Met 165	Pro	Phe	Met	Ile	His 170	Gln	Leu	Met	Gly	Asn 175	Gly
Val	Trp	His	Phe 180	Gly	Glu	Thr	Met	Cys 185	Thr	Leu	Ile	Thr	Ala 190	Met	Asp
Ala	Asn	Ser 195	Gln	Phe	Thr	Ser	Thr 200	Tyr	Ile	Leu	Thr	Ala 205	Met	Ala	Ile
Asp	Arg 210	Tyr	Leu	Ala	Tnr	Val 215	His	Pro	Ile	Ser	Ser 220	Thr	Lys	Phe	Arg
Lys 225	Pro	Ser	Val	Ala	Thr 230	Leu	Val	Ile	Cys	Leu 235	Leu	Trp	Ala	Leu	Ser 240
Phe	Ile	Ser	Ile	Thr 245	Pro	Val	Trp	Leu	Tyr 250	Ala	Arg	Leu	Ile	Pro 255	Phe
Pro	Gly	Gly	Ala 260	Val	Gly	Cys	Gly	Ile 265	Arg	Leu	Pro	Asn	Pro 270	Asp	Thr
Asp	Leu	Tyr 275	Trp	Phe	Thr	Leu	Tyr 280	Gln	Phe	Phe	Leu	Ala 285	Phe	Ala	Leu
Pro	Phe 290	Val	Val	Ile	Thr	Ala 295	Ala	Tyr	Val	Arg	Ile 300	Leu	Gln	Arg	Met
Thr 305	Ser	Ser	Val	Ala	Pro 310	Ala	Ser	Gln	Arg	Ser 315	Ile	Arg	Leu	Arg	Thr 320
Lys	Arg	Val	Thr	Arg 325	Thr	Ala	Ile	Ala	Ile 330	Cys	Leu	Val	Phe	Phe 335	Val
Cys	Trp	Ala	Pro 340	Tyr	Tyr	Val	Leu	Gln 345	Leu	Thr	Gln	Leu	Ser 350	Ile	Ser
Arg	Pro	Thr 355	Leu	Thr	Phe	Val	Tyr 360	Leu	Tyr	Asn	Ala	Ala 365	Ile	Ser	Leu
Gly	Tyr 370	Ala	Asn	Ser	Cys	Leu 375	Asn	Pro	Phe	Val	Tyr 380	Ile	Val	Leu	Cys
Glu 385	Thr	Phe	Arg	Lys	Arg 390	Leu	Val	Leu	Ser	Val 395	Lys	Pro	Ala	Ala	Gln 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg 405 410 415

Thr Glu Ser Lys Gly Thr 420

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: mutated human MCH1

<400> 28

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Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met · 100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly

165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180 185 190

- Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195 200 205
- Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210 215 220
- Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser 225 230 235 240
- Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe 245 250 255
- Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr 260 265 270
- Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu 275 280 285
- Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met 290 295 300
- Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr 305 310 315 320
- Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val 325 330 335
- Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser 340 345 350
- Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu 355 360 365
- Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys 370 375 380
- Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln 385 390 395 400
- Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
 405 410 415

Thr Glu Ser Lys Gly Thr

<210> 29

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human MCH1

<400> 29

Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn 1 5 10 15

Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg 20 25 30

Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly 35 40 45

Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala 50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile 65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met 85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly 100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe 115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala 130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala 145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr 165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val 180 185 190

- Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe 195 200 205
- Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile 210 225 220
- Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala 225 230 235 240
- Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg 245 250 255
- Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr 260 265 270
- Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr 275 280 285
- Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser 290 295 300
- Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys 305 310 315
- Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala 325 330 335
- Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly 340 345 350

Thr